

Run on: August 17, 2005, 18:01:27 ; Search time 3856 Seconds
(without alignments)

Title: US-10-021-753A-1

Sequence: 1 ccccccagagcgcctcgcg.....catttaactcatttgagag 836

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 20

Total number of hits satisfying chosen parameters: 591

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Listing first 45 summaries

Database: GenEmbl:*

1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sls:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Match	Length	DB	ID	Description
1	830	100.0	830	6	BD186306	BD186306 STAT6 act
2	830	100.0	830	6	AX337063	AX337063 Sequence
3	830	100.0	830	9	HSTLMP	X16064 Human mRNA
4	829	99.9	830	6	AX500153	AX500153 Sequence
5	829	99.9	831	6	CQ728369	CQ728369 Sequence
6	821	98.9	840	9	BC003352	BC003352 Homo sapi
7	821	98.9	855	9	BC062333	BC062333 Homo sapi
8	820	98.8	841	9	AK130847	AK130847 Homo sapi
9	814	98.1	866	9	AY117678	AY117678 Homo sapi
10	740	84.3	818	9	BC012431	BC012431 Homo sapi
11	645	77.7	645	6	CQ833420	CQ833420 Sequence
12	634	76.4	1134	9	BC022436	BC022436 Homo sapi

13	509	73.4	938	6	AX406753	AX405763 Sequence
14	677	69.5	599	6	AX381150	AX381150 Sequence
15	563	67.8	563	9	HUdMCH1304A	L13806 Homo sapien
16	539	64.9	539	6	CQ671453	CQ671453 Sequence
17	519	62.5	519	6	AX806477	AX806477 Sequence
c 18	519	62.5	519	6	AX356373	AX356373 Sequence
19	519	62.5	519	9	CR457036	CR457036 Homo sapi
20	519	62.5	577	6	AX381508	AX381508 Sequence
21	516	62.2	516	6	BD142401	BD142401 Homo sapi
22	512	61.7	819	9	HSNMF21HOM	X64899 H. insulans m
23	501	60.4	519	9	AX734563	AX734563 Homo sapi
24	496	56.8	506	6	AX393798	AX393798 Sequence
c 25	480	57.8	531	6	AX396759	AX396759 Sequence
26	478	57.2	499	6	CQ713515	CQ713515 Sequence
27	474	57.1	535	6	AX396495	AX396495 Sequence
28	465	56.0	465	6	CQ691284	CQ691284 Sequence
29	465	56.0	465	6	CQ693052	CQ693052 Sequence
30	457	55.1	471	6	AX340927	AX340927 Sequence
31	456	54.9	467	6	AX339997	AX339997 Sequence
32	453	54.6	465	6	CQ693930	CQ693930 Sequence
33	445	53.6	447	6	CQ679650	CQ679650 Sequence
34	440	53.0	469	6	CQ696611	CQ696611 Sequence
35	439	52.9	890	6	AX283790	AX283790 Sequence
36	433	52.2	467	6	CQ713036	CQ713036 Sequence
37	431	51.9	472	6	CQ683000	CQ683000 Sequence
38	429	51.7	632	6	AX198550	AX198550 Sequence
39	429	51.7	632	6	AX209119	AX209119 Sequence
40	425	51.2	433	6	AX393787	AX393787 Sequence
41	424	51.1	424	6	CQ663748	CQ663748 Sequence
c 42	420	50.6	420	6	AX397225	AX397225 Sequence
43	420	50.6	670	6	CQ693950	CQ693950 Sequence
44	411	49.5	513	6	AX393690	AX393690 Sequence
45	409	49.3	522	6	AX396097	AX396097 Sequence

ALIGNMENTS

RESULT 1

LOCUS	BD186306	830 bp	DNA	linear	PAT 17-JUN-2003
DEFINITION	STAT1B activating gene.				
ACCESSION	BD186306				
VERSION	BD186306.1	GI:3187806.			
KEYWORDS	WO 02096343-A173.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				

REFERENCE 1 (bases 1 to 830)
Mammalia: Euthera: Primates: Catarrhini: Homiidae: Homo.
Eukaryota: Metazoa: Chordata: Gracilata: Vertebrata: Euteleostomi:
AUTHORS Honda G., Matsuda A., Muramatsu S. and Ishizawa K.
TITLE STATA6 activating gene
JOURNAL Patent: WO 02/056543-A 175 05-DEC-2002;

ASAH KASEI CORP, GOICHI HONDA, AKIO MATSUDA, SHUJI MURAMATSU, KENTA
ISHIZAWA
COMMENT OS Homo sapiens (human)

PN WO 0209643-A/175
PD 05-DEC-2002
PR 23-MAY-2002 WO 2002/JP004949
PR 25-MAY-2001 JP 01P 157043.30-A/UG-2001 JP 01P 280681 PR
10-OCT-2001 JP 01P 313175
PI GOICHI HONDA,AKIO MATSUDA,SHUJI MURAMATSU,KENYA ISHIZAWA PC
C07K14/47,C07K17/00,C12N16/12,C12N5/10,C12P21/02,C12P21/08, PC
C12Q1/02
PC A61P3/06,A61P3/10,A61P29/00,A61P31/00,A61P35/00,A61P37/00, PC
G01N33/15,

GenCore version 5.1.6
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Run on: August 17, 2005, 17:41:12 ; Search time 559 Seconds
(without alignments)
8789.598 Million cell updates/sec

Title: US-10-021-753A-1
Perfect score: 830
Sequence: 1 ccccccgcagcgcctcgcg.....catttaactcatttgagag 830

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 20

Total number of hits satisfying chosen parameters: 274

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Minimum DB seq length: 0
Maximum DB seq length: 1000000000
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Post-processing: Listing first 45 summaries

Database: N_Geneseq_16Dec04.*

- 1: geneseqn1985s.*
- 2: geneseqn1990s.*
- 3: geneseqn2000s.*
- 4: geneseqn2001as.*
- 5: geneseqn2001bs.*
- 6: geneseqn2002as.*
- 7: geneseqn2002bs.*
- 8: geneseqn2003as.*
- 9: geneseqn2003bs.*
- 10: geneseqn2003cs.*
- 11: geneseqn2003ds.*
- 12: geneseqn2004as.*
- 13: geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	No. Match	Length	DB ID	Description
1	830 100.0	830.6	ABL69235		ABl69235 Prostate
2	830 100.0	830.6	ABK94540		Abk94540 Human cDN
3	830 100.0	830.6	ABK98326		Abk98326 Human For
4	830 100.0	830.8	ADX10438		Abx10438 DNA encod
5	830 100.0	830.0	ADT010769		ADT010769 Human STPA
6	830 100.0	830.3	ACN939630		Acn939630 Tumour as
7	830 100.0	838.2	AAQ666875		Aaq66675 Tumor pro
8	829 99.9	830.8	ABX6594		Abx65994 Gene encod
9	821 98.9	852.0	ADG32861		Adg32861 Human DNA
10	821 98.9	1235.0	ADG08987		Adg08987 Novel DNA
11	810 97.6	810.0	ADH85755		Adh85755 Human ade

15	422	50.8	423.9	ACHI18358
44	425	51.2	433.5	ABH5381
43	429	51.7	432.5	AAH5341
42	438	52.8	466.9	AAH54178
41	439	52.8	466.9	AAH54178
40	439	52.9	466.9	AAH54178
39	439	52.9	466.9	AAH54178
38	441	53.1	480.9	ACH24859
37	452	54.5	502.9	ACH33708
36	456	54.9	507.6	ACH36655
35	457	55.1	471.6	ACH34095
34	458	55.2	508.9	ACH34095
33	461	55.5	490.6	ABV87148
32	465	56.0	703.6	ABV80526
31	470	56.6	521.6	ABV87714
30	474	57.1	535.6	ABK45453
29	480	57.8	531.6	ABK45453
28	486	59.8	506.6	ABK39392
27	516	62.2	516.6	ABK49328
26	519	62.5	577.6	ABK4976
25	519	62.5	519.12	ADDE56584
24	519	62.5	519.10	ADDE26670
23	532	64.1	532.6	ABV87963
22	543	65.4	976.10	AD5071129
21	570	68.7	657.5	AAK90322
20	577	69.8	616.8	ABZ20317
19	579	69.8	616.8	ABZ20317
18	596	71.1	590.6	AAV868032
17	596	71.1	590.6	AAV868032
16	609	73.4	938.6	ABN56976
15	622	74.9	823.12	AD584479
14	622	74.9	823.12	ADP02981
13	645	77.7	645.12	ADG921003
12	760	91.6	834.10	ACC759068
11	769	91.6	834.10	ACC759068
10	769	91.6	834.10	ACC759068
9	769	91.6	834.10	ACC759068
8	769	91.6	834.10	ACC759068
7	769	91.6	834.10	ACC759068
6	769	91.6	834.10	ACC759068
5	769	91.6	834.10	ACC759068
4	769	91.6	834.10	ACC759068
3	769	91.6	834.10	ACC759068
2	769	91.6	834.10	ACC759068
1	769	91.6	834.10	ACC759068

ALIGNMENTS

RESULT 1	
ABL69235	
ID	ABL69235 standard: DNA: 830 BP.
XX	
AC	ABL69235;
XX	
DJ	15-MAY-2002 (first entry)
XX	
DE	Prostate cancer related gene sequence SEQ ID NO:7572.
XX	
KW	Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW	stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW	cytotoxic; gene therapy; antineoplastic; Wilms' tumour; adenocarcinoma;
KW	gene; Os.
XX	
OS	Homo sapiens.
XX	
PN	WO200194629-A2.
XX	
PD	13-DEC-2001.
XX	
PF	30-MAY-2001; 2001WO-US010838.
XX	
PR	05-JUN-2000; 2000US-0209473P.
PR	05-JUN-2000; 2000US-0209531P.
PR	18-SEP-2000; 2000US-0233133P.
RR	18-SEP-2000; 2000US-0233617P.